

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Gately, Maurice K. Presky, David H.
- (ii) TITLE OF INVENTION: ANTIBODIES AGAINST HUMAN IL-12
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Hoffmann-La Roche Inc.
 - (B) STREET: 340 Kingsland Street
 - (C) CITY: Nutley
 - (D) STATE: New Jersey
 - (E) COUNTRY: United States
 - (F) ZIP: 07110-1199
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Buchholz, Briana C.
 - (B) REGISTRATION NUMBER: 39,123
 - (C) REFERENCE/DOCKET NUMBER: CD 1048P
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 973-235-6208
 - (B) TELEFAX: 973-235-2363
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 321 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO

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	(ix)	()	ATURI A) NI B) L	AME/I			321						
	(xi) SE	QUEN	CE DI	ESCR	IPTI	ON:	SEQ :	ID NO	0:1:			
			TCA Ser										48
			TCT Ser 20										96
			AAA Lys										144
			GGT Gly										192
			CGA Arg										240
			ACT Thr										288
			GAC Asp										321

(2) INFORMATION FOR SEQ ID NO:2:

100

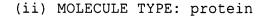
(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 107 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear



105



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Leu Glu Glu Ser Gly Pro Ser Leu Val Lys Pro Ser Gln Thr Leu Ser
1 5 10 15

Leu Thr Cys Ser Val Thr Gly Asp Ser Ile Thr Ser Gly Tyr Trp Asn 20 25 30

Trp Ile Arg Lys Phe Pro Gly Asn Lys Phe Glu Tyr Met Gly Phe Ile 35 40 45

Ser Tyr Ser Gly Ser Thr Tyr Asn Asn Pro Ser Leu Lys Asn Arg Val
50 55 60

Ser Ile Thr Arg Asp Thr Ser Asn Asn Gln Tyr Tyr Leu Gln Leu Ser 65 70 75 80

Ser Val Thr Thr Glu Asp Ser Ala Thr Tyr Tyr Cys Ala Arg Ser Ser 85 90 95

Asp Ala Leu Asp Tyr Trp Gly Ala Gly Thr Thr
100 105

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 308 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: mouse
 - (G) CELL TYPE: Hybridoma
 - (H) CELL LINE: HIL-12F3-20E11
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..306
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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						CTC Leu										48
						GAC Asp										96
						AAT Asn										144
						TAC Tyr 55										192
						AAG Lys										240
						GCC Ala										288
				TGG Trp		GC										308
(2)	INFO	INFORMATION FOR			SEQ	SEQ ID NO:4:										
	(i) SEOUENCE					CHARACTERISTICS										

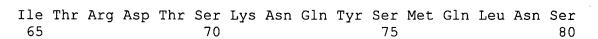
- - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Glu Glu Ser Gly Pro Ser Leu Val Lys Pro Ser Gln Thr Leu Ser Leu 10

Thr Cys Ser Val Thr Gly Asp Ser Ile Thr Ser Gly Tyr Trp Asn Trp 25

Ile Arg Lys Phe Pro Asp Asn Thr Leu Glu Tyr Met Gly Tyr Ile Ser 35 45

Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser Leu Arg Ser Arg Ile Ser 55 60



Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Ser Ser Asp 85 90 95

Ala Met Asp Tyr Trp Gly 100